

(FILE 'HOME' ENTERED AT 15:28:44 ON 31 JUL 2006)

STM/AS

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE' ENTERED AT 15:28:58 ON 31 JUL 2006

L1 241 S CISMOWSKI?/AU OR DUZIC?/AU
L2 49 S L1 AND (ACTIVATOR(3A)G PROTEIN)
L3 23 DUP REM L2 (26 DUPLICATES REMOVED)
L4 3463 S (ACTIVATOR OR REGULATOR) (3A) G PROTEIN (3A)SIGNALING
L5 132 S L4 AND PHEROMONE
L6 55 DUP REM L5 (77 DUPLICATES REMOVED)
L7 5248 S DEXAMETHASONE INDUCED
L8 0 S LD RAS RELATED PROTEIN
L9 9 S L7 AND RAS RELATED PROTEIN
L10 4 DUP REM L9 (5 DUPLICATES REMOVED)
L11 100 S DEXRAS1
L12 41 DUP REM L11 (59 DUPLICATES REMOVED)
L13 17552 S AGS?
L14 331 S L13 AND G PROTEIN
L15 35 S L14 NOT PY>1999
L16 14 DUP REM L15 (21 DUPLICATES REMOVED)

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	20	ags1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:18
L2	6	L1 and "g protein"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:18
L3	9	dexras1	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:18
L4	236	ags same protein	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:21
L6	9	L4 same mammal\$5	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:19
L7	28	dexamethasone near5 ras	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:19
L8	8	dexamethasone.clm. and ras.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:21
L9	2	dexras1.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:20
L11	92	ags\$3.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:21
L12	4	L11 same protein	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:21
L13	236	ags same protein	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:27

EAST Search History

L14	0	rasd1.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:27
L15	0	ags1.clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/07/31 15:27

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.p2n.rge.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:34 ; Search time 6789.62 Seconds
(without alignments)
3969.861 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100916_16816/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10804491@CGN_1_1_6250@runat_26072006_100916_16816 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	%	Match	Length	DB	ID	Description
No.	Score						

1	1449	100.0	846	2	AR534270	AR534270 Sequence
2	1449	100.0	846	2	AR544556	AR544556 Sequence
3	1449	100.0	846	5	AF498923	AF498923 Homo sapi
4	1449	100.0	979	5	AF172846	AF172846 Homo sapi
5	1449	100.0	1187	5	AF153192	AF153192 Homo sapi
6	1449	100.0	1188	5	CQ724730	CQ724730 Sequence
7	1449	100.0	1740	2	AR534303	AR534303 Sequence
8	1449	100.0	1740	2	AR544589	AR544589 Sequence
9	1449	100.0	1740	2	AX780438	AX780438 Sequence
10	1449	100.0	1740	5	AF069506	AF069506 Homo sapi
11	1449	100.0	1744	2	BD190304	BD190304 Elk1 phos
12	1449	100.0	1758	2	CQ981517	CQ981517 Sequence
13	1449	100.0	1758	2	CS129182	CS129182 Sequence
14	1449	100.0	1758	5	BC018041	BC018041 Homo sapi
15	1449	100.0	1801	2	AR534271	AR534271 Sequence
16	1449	100.0	1801	2	AR544557	AR544557 Sequence
17	1449	100.0	1841	2	AR236058	AR236058 Sequence
18	1441	99.4	1776	2	BD248751	BD248751 GTPase as
19	1436	99.1	1746	5	AF177335	AF177335 Homo sapi
20	1405.5	97.0	843	6	CT010376	CT010376 Mus muscu
21	1405.5	97.0	1612	6	BC034166	BC034166 Mus muscu
22	1405.5	97.0	1623	6	AF009246	AF009246 Mus muscu
23	1399.5	96.6	1592	6	BC099136	BC099136 Rattus no
24	1399.5	96.6	1616	6	AF239157	AF239157 Rattus no
25	1399.5	96.6	1689	2	AR236060	AR236060 Sequence
26	1387	95.7	3986	2	AR236059	AR236059 Sequence
27	1387	95.7	4990	2	AR544590	AR544590 Sequence
28	1387	95.7	4990	5	AF222979	AF222979 Homo sapi
29	1387	95.7	141048	5	AC073621	AC073621 Homo sapi
c 30	1387	95.7	183334	5	AC020558	AC020558 Homo sapi
31	1387	95.7	183427	12	AC090608	AC090608 Homo sapi
32	1384	95.5	5141	5	AF262018	AF262018 Homo sapi
c 33	1370	94.5	179124	6	AL603710	AL603710 Mouse DNA
c 34	1370	94.5	247899	12	AC025909	AC025909 Mus muscu
35	1343	92.7	3079	2	AR236061	AR236061 Sequence
c 36	1343	92.7	314307	12	AC122995	AC122995 Rattus no
37	1242.5	85.7	1396	14	BC103301	BC103301 Bos tauru
c 38	1177	81.2	234274	12	AC162419	AC162419 Bos tauru
39	1169	80.7	1383	11	BC081268	BC081268 Xenopus l
40	1144.5	79.0	1390	11	BC056272	BC056272 Danio rer
41	1139.5	78.6	220633	12	AC170448	AC170448 Bos tauru
42	917	63.3	2381	11	CR848237	CR848237 Xenopus t
43	910	62.8	1702	11	BX933149	BX933149 Gallus ga
44	905	62.5	2430	11	BC074172	BC074172 Xenopus l
45	893	61.6	810	2	CQ730256	CQ730256 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:08:51 ; Search time 742.643 Seconds
(without alignments)
3957.222 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100914_16805/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491@CGN_1_1_942@runat_26072006_100914_16805 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1449	100.0	846	3	AAZ36892	Aaz36892 cDNA enco
2	1449	100.0	846	14	ADV44056	Adv44056 Human psy
3	1449	100.0	1740	3	AAZ36914	Aaz36914 DNA encod
4	1449	100.0	1740	10	ADF82039	Adf82039 Leukaemia
5	1449	100.0	1740	12	ADP21394	Adp21394 Gene RASD
6	1449	100.0	1744	8	ACC42325	Acc42325 Human MAP
7	1449	100.0	1758	13	ADU06148	Adu06148 Novel bro
8	1449	100.0	1801	3	AAZ36893	Aaz36893 cDNA enco
9	1449	100.0	1841	2	AAZ23022	Aaz23022 Human kd3
10	1441	99.4	1776	3	AAA49177	Aaa49177 cDNA enco
11	1399.5	96.6	1689	2	AAZ23024	Aaz23024 Rat kd312
12	1387	95.7	3986	2	AAZ23023	Aaz23023 Human kd3
13	1343	92.7	3079	2	AAZ23025	Aaz23025 Rat kd312
14	1064	73.4	649	10	ADD34625	Add34625 Mouse mit
15	893	61.6	837	3	AAZ36913	Aaz36913 DNA encod
16	893	61.6	2832	6	ABL92076	Abl92076 Human Tum
17	893	61.6	2832	10	ABX72001	Abx72001 DNA encod
18	893	61.6	2832	12	ADI66873	Adi66873 Human DEX
19	893	61.6	2973	6	ABL92087	Abl92087 Human Tum
20	893	61.6	2973	10	ABX72012	Abx72012 DNA encod
21	893	61.6	3058	12	ADQ22314	Adq22314 Human sof
22	893	61.6	3427	6	ABK71563	Abk71563 Human dit
23	883	60.9	3082	6	ABS54600	Abs54600 cDNA enco
24	867	59.8	3020	6	ABL92134	Abl92134 Mouse Tum
25	867	59.8	3020	10	ABX72059	Abx72059 DNA encod
26	717	49.5	951	5	AAS90571	Aas90571 DNA encod
27	615	42.4	1305	4	ABL07789	Abl07789 Drosophil
28	526	36.3	11221	6	ABS54740	Abs54740 Genomic D
29	526	36.3	16000	12	ADI66880	Adi66880 Human DEX
30	526	36.3	114771	12	ADQ17641	Adq17641 Human sof
31	517	35.7	696	12	ACH87756	Ach87756 Human gen
32	494	34.1	624	6	ABQ28318	Abq28318 Oligonucl
c 33	494	34.1	624	6	ABQ28319	Abq28319 Oligonucl
34	485	33.5	405	8	ABX45108	Abx45108 Bovine ES
35	464	32.0	523	12	ADI66881	Adi66881 Human DEX
c 36	459	31.7	624	6	ABQ28320	Abq28320 Oligonucl
37	459	31.7	624	6	ABQ28321	Abq28321 Oligonucl
38	370	25.5	368	4	AAI24259	Aai24259 Probe #14
39	370	25.5	368	4	ABA69388	Aba69388 Human foe
40	370	25.5	368	4	AAI49541	Aai49541 Probe #18
41	370	25.5	368	4	ABA51382	Aba51382 Human bre
42	370	25.5	368	4	ABA36323	Aba36323 Probe #14
43	370	25.5	368	4	AAK43477	Aak43477 Human bon
44	370	25.5	368	4	AAK17661	Aak17661 Human bra
45	370	25.5	368	4	ABS43113	Abs43113 Human liv

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:01 ; Search time 225.043 Seconds
(without alignments)
3504.536 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100921_16893/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss05h -USER=US10804491 @CGN_1_1_252 @runat_26072006_100921_16893
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	846	3	US-09-709-103-1
2	1449	100.0	846	3	US-09-439-410A-1
3	1449	100.0	1740	3	US-09-709-103-45
4	1449	100.0	1740	3	US-09-439-410A-45
5	1449	100.0	1801	3	US-09-709-103-3

6	1449	100.0	1801	3	US-09-439-410A-3	Sequence 3, Appli
7	1449	100.0	1841	3	US-09-053-374A-1	Sequence 1, Appli
8	1399.5	96.6	1689	3	US-09-053-374A-4	Sequence 4, Appli
9	1387	95.7	3986	3	US-09-053-374A-3	Sequence 3, Appli
10	1387	95.7	4990	3	US-09-439-410A-73	Sequence 73, Appl
11	1343	92.7	3079	3	US-09-053-374A-6	Sequence 6, Appli
12	893	61.6	837	3	US-09-709-103-40	Sequence 40, Appl
13	893	61.6	837	3	US-09-439-410A-40	Sequence 40, Appl
14	893	61.6	837	3	US-09-949-016-5022	Sequence 5022, Ap
15	883	60.9	3082	4	US-09-778-963B-1	Sequence 1, Appli
16	526	36.3	9259	3	US-09-949-016-16764	Sequence 16764, A
17	526	36.3	11221	4	US-09-778-963B-3	Sequence 3, Appli
18	334	23.1	1108	3	US-09-620-312D-945	Sequence 945, App
19	302	20.8	3300	3	US-09-620-312D-456	Sequence 456, App
20	300	20.7	615	2	US-08-247-946A-5	Sequence 5, Appli
21	300	20.7	615	7	PCT-US95-06420-5	Sequence 5, Appli
22	282.5	19.5	1368	3	US-09-949-016-4767	Sequence 4767, Ap
23	280	19.3	567	3	US-09-223-588-1	Sequence 1, Appli
24	279	19.3	5775	2	US-08-306-691B-15	Sequence 15, Appl
25	279	19.3	5775	3	US-09-023-655-1145	Sequence 1145, Ap
26	279	19.3	5775	3	US-09-949-016-702	Sequence 702, App
27	279	19.3	5775	7	PCT-US93-06251-29	Sequence 29, Appl
28	278.5	19.2	432	3	US-09-621-976-17745	Sequence 17745, A
29	278	19.2	567	3	US-09-223-588-2	Sequence 2, Appli
30	277.5	19.2	570	3	US-08-884-866A-2	Sequence 2, Appli
31	277.5	19.2	570	3	US-08-884-866A-11	Sequence 11, Appl
32	276	19.0	607	2	US-08-429-964-85	Sequence 85, Appl
33	275.5	19.0	480	3	US-08-884-866A-9	Sequence 9, Appli
34	275.5	19.0	551	3	US-09-765-298A-25	Sequence 25, Appl
35	272.5	18.8	570	3	US-09-765-298A-27	Sequence 27, Appl
36	271.5	18.7	4480	3	US-09-167-322-12	Sequence 12, Appl
37	266.5	18.4	450	3	US-08-884-866A-10	Sequence 10, Appl
38	266.5	18.4	574	2	US-08-429-964-83	Sequence 83, Appl
39	265.5	18.3	2436	2	US-08-306-691B-16	Sequence 16, Appl
40	264.5	18.3	930	3	US-09-487-558B-285	Sequence 285, App
41	256.5	17.7	711	3	US-09-248-796A-5513	Sequence 5513, Ap
42	251	17.3	798	3	US-09-248-796A-5510	Sequence 5510, Ap
43	245.5	16.9	969	3	US-09-487-558B-287	Sequence 287, App
44	240	16.6	2894	3	US-09-976-594-842	Sequence 842, App
45	237	16.4	2309	3	US-09-078-317-3	Sequence 3, Appli

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.p2n.rnpbm.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 15:25:55 ; Search time 1501.1 Seconds
(without alignments)
3450.296 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKKMCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100930_17074/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491_CGN_1_1_2326@runat_26072006_100930_17074 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

No.	Score	Match	Length	DB	ID	Description
1	1449	100.0	846	9	US-10-804-491-1	Sequence 1, Appli
2	1449	100.0	1740	9	US-10-804-491-45	Sequence 45, Appl
3	1449	100.0	1744	6	US-10-197-666A-87	Sequence 87, Appl
4	1449	100.0	1758	10	US-10-956-157-2062	Sequence 2062, Ap
5	1449	100.0	1801	9	US-10-804-491-3	Sequence 3, Appli
6	1204	83.1	1400	10	US-10-956-157-7297	Sequence 7297, Ap
7	893	61.6	837	9	US-10-804-491-40	Sequence 40, Appl
8	893	61.6	2832	3	US-09-918-715-174	Sequence 174, App
9	893	61.6	2832	7	US-10-185-035-4	Sequence 4, Appli
10	893	61.6	2832	9	US-10-474-794-174	Sequence 174, App
11	893	61.6	2832	10	US-10-979-159-174	Sequence 174, App
12	893	61.6	2973	3	US-09-918-715-197	Sequence 197, App
13	893	61.6	2973	9	US-10-474-794-197	Sequence 197, App
14	893	61.6	2973	10	US-10-979-159-197	Sequence 197, App
15	893	61.6	3058	9	US-10-723-860-5134	Sequence 5134, Ap
16	883	60.9	3082	3	US-09-778-963A-1	Sequence 1, Appli
17	867	59.8	3020	3	US-09-918-715-292	Sequence 292, App
18	867	59.8	3020	9	US-10-474-794-292	Sequence 292, App
19	867	59.8	3020	10	US-10-979-159-292	Sequence 292, App
20	717	49.5	951	10	US-10-450-763-26375	Sequence 26375, A
21	615	42.4	1305	13	US-11-097-143-8924	Sequence 8924, Ap
22	526	36.3	11221	3	US-09-778-963A-3	Sequence 3, Appli
23	526	36.3	16000	7	US-10-185-035-11	Sequence 11, Appl
24	526	36.3	114771	9	US-10-723-860-458	Sequence 458, App
25	517	35.7	696	7	US-10-029-386-20951	Sequence 20951, A
26	494	34.1	624	9	US-10-363-345A-14909	Sequence 14909, A
c 27	494	34.1	624	9	US-10-363-345A-14910	Sequence 14910, A
28	494	34.1	624	10	US-10-363-483A-14909	Sequence 14909, A
c 29	494	34.1	624	10	US-10-363-483A-14910	Sequence 14910, A
30	485	33.5	405	3	US-09-960-352-10273	Sequence 10273, A
31	464	32.0	523	7	US-10-185-035-12	Sequence 12, Appl
c 32	459	31.7	624	9	US-10-363-345A-14911	Sequence 14911, A
33	459	31.7	624	9	US-10-363-345A-14912	Sequence 14912, A
c 34	459	31.7	624	10	US-10-363-483A-14911	Sequence 14911, A
35	459	31.7	624	10	US-10-363-483A-14912	Sequence 14912, A
36	370	25.5	368	3	US-09-864-761-21643	Sequence 21643, A
37	359.5	24.8	4543	13	US-11-097-143-8923	Sequence 8923, Ap
38	334	23.1	1108	6	US-10-037-270-945	Sequence 945, App
39	334	23.1	1108	7	US-10-117-722-945	Sequence 945, App
40	334	23.1	1108	10	US-10-122-851-945	Sequence 945, App
41	334	23.1	4167	8	US-10-399-456-36	Sequence 36, Appl
42	330.5	22.8	960	13	US-11-097-143-31052	Sequence 31052, A
43	326	22.5	597	3	US-09-873-546-4	Sequence 4, Appli
c 44	326	22.5	597	7	US-10-029-386-22936	Sequence 22936, A
45	326	22.5	3440	9	US-10-723-860-8257	Sequence 8257, Ap

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.p2n.rnpbn.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 15:30:26 ; Search time 377.1 Seconds
(without alignments)
1708.556 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMCPSPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100933_17116/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491_CGN_1_1_278_@runat_26072006_100933_17116 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	1758	8	US-11-266-748A-30197 Sequence 30197, A
2	1384	95.5	5141	8	US-11-266-748A-23441 Sequence 23441, A
3	1143	78.9	796	8	US-11-266-748A-227676 Sequence 227676, A
4	1142	78.8	1133	8	US-11-266-748A-98774 Sequence 98774, A
c 5	1142	78.8	1133	8	US-11-266-748A-151585 Sequence 151585, A

	6	1064	73.4	649	6	US-10-488-619-2403	Sequence 2403, Ap
	7	893	61.6	2832	8	US-11-266-748A-23473	Sequence 23473, A
	8	883	60.9	1044	8	US-11-266-748A-98494	Sequence 98494, A
c	9	883	60.9	1044	8	US-11-266-748A-151305	Sequence 151305,
	10	580	40.0	445	8	US-11-266-748A-1108	Sequence 1108, Ap
	11	326	22.5	597	8	US-11-266-748A-391090	Sequence 391090,
c	12	326	22.5	597	8	US-11-266-748A-481808	Sequence 481808,
	13	307.5	21.2	1021	6	US-10-354-953-158	Sequence 158, App
	14	306	21.1	552	8	US-11-266-748A-61269	Sequence 61269, A
	15	305	21.0	820	8	US-11-266-748A-219154	Sequence 219154,
c	16	305	21.0	820	8	US-11-266-748A-239354	Sequence 239354,
	17	305	21.0	6237	8	US-11-266-748A-29324	Sequence 29324, A
	18	303	20.9	3227	8	US-11-266-748A-25347	Sequence 25347, A
	19	302	20.8	570	8	US-11-266-748A-92453	Sequence 92453, A
	20	302	20.8	570	8	US-11-266-748A-113007	Sequence 113007,
c	21	302	20.8	570	8	US-11-266-748A-145264	Sequence 145264,
	22	302	20.8	4121	8	US-11-266-748A-28133	Sequence 28133, A
	23	302	20.8	4370	8	US-11-266-748A-27348	Sequence 27348, A
	24	301	20.8	2264	6	US-10-539-228-466	Sequence 466, App
	25	301	20.8	2297	6	US-10-539-228-473	Sequence 473, App
	26	300	20.7	2370	8	US-11-266-748A-27004	Sequence 27004, A
	27	290	20.0	2406	6	US-10-539-228-70	Sequence 70, Appl
	28	288.5	19.9	819	8	US-11-217-529-76787	Sequence 76787, A
	29	283.5	19.6	924	8	US-11-266-748A-227367	Sequence 227367,
	30	283.5	19.6	1103	8	US-11-266-748A-15208	Sequence 15208, A
	31	283.5	19.6	1407	8	US-11-266-748A-186675	Sequence 186675,
	32	283.5	19.6	1407	8	US-11-266-748A-193853	Sequence 193853,
	33	283.5	19.6	2314	6	US-10-539-228-77	Sequence 77, Appl
	34	282.5	19.5	819	8	US-11-217-529-1017	Sequence 1017, Ap
	35	282.5	19.5	1294	6	US-10-539-228-821	Sequence 821, App
c	36	282.5	19.5	1480	8	US-11-266-748A-19818	Sequence 19818, A
	37	282.5	19.5	1480	8	US-11-266-748A-62399	Sequence 62399, A
c	38	282.5	19.5	1480	8	US-11-266-748A-65238	Sequence 65238, A
	39	282	19.5	1000	8	US-11-266-748A-116584	Sequence 116584,
c	40	282	19.5	1000	8	US-11-266-748A-158748	Sequence 158748,
	41	282	19.5	1000	8	US-11-266-748A-221835	Sequence 221835,
	42	281	19.4	1333	8	US-11-266-748A-25940	Sequence 25940, A
	43	280	19.3	934	8	US-11-266-748A-9975	Sequence 9975, Ap
	44	280	19.3	5312	8	US-11-266-748A-29561	Sequence 29561, A
c	45	279.5	19.3	1331	8	US-11-266-748A-175445	Sequence 175445,

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.p2n.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:39 ; Search time 5719.14 Seconds
(without alignments)
4121.248 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100918_16839/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10804491@CGN_1_1_7986@runat_26072006_100918_16839 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	1694	6 CR596563	CR596563 full-leng

	2	1449	100.0	1780	6	BC042688	BC042688 Homo sapi
	3	1405.5	97.0	1474	6	AK038932	AK038932 Mus muscu
	4	1352.5	93.3	834	5	CD513046	CD513046 AGENCOURT
	5	1297.5	89.5	812	8	CX230968	CX230968 MBM07758
	6	1262	87.1	822	5	CD251380	CD251380 AGENCOURT
	7	1243	85.8	914	5	CD513372	CD513372 AGENCOURT
	8	1242.5	85.7	887	10	DT808732	DT808732 LB0161.CR
	9	1226.5	84.6	743	8	CV104818	CV104818 AGENCOURT
	10	1210.5	83.5	1035	3	BM919341	BM919341 AGENCOURT
	11	1193	82.3	836	10	DT398153	DT398153 JGI_CABI2
	12	1193	82.3	843	10	DT405753	DT405753 JGI_CABI7
	13	1193	82.3	886	4	BX704490	BX704490 BX704490
	14	1191.5	82.2	919	10	DV934170	DV934170 LB0306.CR
c	15	1180	81.4	848	10	DT404262	DT404262 JGI_CABI6
	16	1169	80.7	821	9	CX972499	CX972499 JGI_CAAP7
	17	1165	80.4	962	2	BM543472	BM543472 AGENCOURT
	18	1164	80.3	814	9	CX965491	CX965491 JGI_CAAP1
	19	1144	79.0	1103	3	BM920514	BM920514 AGENCOURT
	20	1136	78.4	780	9	DN068935	DN068935 JGI_CABD5
	21	1136	78.4	780	9	DN073551	DN073551 JGI_CABD7
	22	1136	78.4	786	10	DT404263	DT404263 JGI_CABI6
	23	1136	78.4	800	10	DT405203	DT405203 JGI_CABI7
	24	1134.5	78.3	689	8	CO395082	CO395082 AGENCOURT
	25	1130	78.0	800	10	DT410692	DT410692 JGI_CABI1
	26	1122	77.4	773	8	CV110404	CV110404 AGENCOURT
	27	1121	77.4	1053	1	AL533318	AL533318 AL533318
	28	1120	77.3	742	7	AW028127	AW028127 wv26c07.x
	29	1119	77.2	978	10	DV002641	DV002641 CNB219-G0
	30	1119	77.2	1432	9	DN723109	DN723109 CNB147-G0
	31	1114.5	76.9	958	3	BQ719566	BQ719566 AGENCOURT
	32	1111	76.7	855	4	CD105429	CD105429 AGENCOURT
	33	1108.5	76.5	824	5	CK684001	CK684001 ZF101-P00
	34	1102.5	76.1	867	10	DT256285	DT256285 JGI_CAAU7
	35	1101	76.0	642	8	CV024008	CV024008 1134 Full1
	36	1100.5	75.9	1053	3	BM921737	BM921737 AGENCOURT
	37	1096	75.6	1091	9	DN707871	DN707871 CLJ73-H11
	38	1095.5	75.6	811	10	DT259819	DT259819 JGI_CAAU9
	39	1091.5	75.3	822	8	CN513172	CN513172 AGENCOURT
	40	1073	74.1	828	10	DW557636	DW557636 EST_ssal_
	41	1062	73.3	828	10	DV913687	DV913687 LB02828.C
	42	1061.5	73.3	759	8	CN500085	CN500085 AGENCOURT
	43	1059	73.1	736	8	CX229349	CX229349 MBM04053
	44	1050.5	72.5	786	9	DN893714	DN893714 nao44d04.
	45	1049.5	72.4	784	10	DT055544	DT055544 AGENCOURT

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.ra1.

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OM protein - protein search, using sw model

Run on: July 26, 2006, 10:59:01 ; Search time 50 Seconds
(without alignments)
491.922 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	281	2	US-09-053-374A-2
2	1449	100.0	281	2	US-09-709-103-2
3	1449	100.0	281	2	US-09-709-103-4
4	1449	100.0	281	2	US-09-709-103-46
5	1449	100.0	281	2	US-09-439-410A-2
6	1449	100.0	281	2	US-09-439-410A-4
7	1449	100.0	281	2	US-09-439-410A-46
8	1399.5	96.6	280	2	US-09-053-374A-5
9	893	61.6	278	2	US-09-709-103-41
10	893	61.6	278	2	US-09-439-410A-41
11	893	61.6	278	2	US-09-949-016-10893
12	889	61.4	266	2	US-09-778-963B-4
13	879	60.7	266	2	US-09-778-963B-2
14	863	59.6	266	2	US-09-778-963B-5
15	311	21.5	60	2	US-09-439-410A-109
16	306	21.1	183	1	US-08-531-525-39
17	306	21.1	183	1	US-08-718-270A-39
18	305	21.0	60	2	US-09-439-410A-82
19	303	20.9	59	2	US-09-439-410A-91
20	301	20.8	183	2	US-09-482-520A-8
21	301	20.8	204	2	US-09-078-317-14
22	301	20.8	204	2	US-09-454-818-14
23	300	20.7	204	1	US-08-247-946A-4

24	300	20.7	204	5	PCT-US95-06420-4	Sequence 4, Appli
25	296.5	20.5	215	1	US-08-531-525-49	Sequence 49, Appl
26	296.5	20.5	215	1	US-08-718-270A-49	Sequence 49, Appl
27	288	19.9	213	2	US-09-503-505A-3	Sequence 3, Appli
28	286.5	19.8	184	1	US-08-531-525-40	Sequence 40, Appl
29	286.5	19.8	184	1	US-08-718-270A-40	Sequence 40, Appl
30	285	19.7	187	2	US-09-078-317-11	Sequence 11, Appl
31	283	19.5	55	2	US-09-439-410A-117	Sequence 117, App
32	282.5	19.5	188	2	US-09-949-016-10638	Sequence 10638, A
33	282	19.5	183	2	US-09-078-317-13	Sequence 13, Appl
34	282	19.5	183	2	US-09-454-818-13	Sequence 13, Appl
35	282	19.5	210	2	US-09-053-374A-7	Sequence 7, Appli
36	281	19.4	218	1	US-08-247-946A-3	Sequence 3, Appli
37	281	19.4	218	5	PCT-US95-06420-3	Sequence 3, Appli
38	280.5	19.4	184	1	US-08-531-525-43	Sequence 43, Appl
39	280.5	19.4	184	1	US-08-718-270A-43	Sequence 43, Appl
40	279	19.3	188	2	US-09-949-016-6573	Sequence 6573, Ap
41	277.5	19.2	189	2	US-08-884-866A-3	Sequence 3, Appli
42	277.5	19.2	189	2	US-08-884-866A-6	Sequence 6, Appli
43	276	19.0	188	1	US-08-429-964-84	Sequence 84, Appl
44	275.5	19.0	160	2	US-08-884-866A-7	Sequence 7, Appli
45	275.5	19.0	183	2	US-09-765-298A-26	Sequence 26, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 11:11:01 ; Search time 186 Seconds
(without alignments)
699.803 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMCPDSELSIP.....IREKASAGSQADKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	281	4	US-10-197-666A-88 Sequence 88, Appl
2	1449	100.0	281	4	US-10-804-491-2 Sequence 2, Appli
3	1449	100.0	281	4	US-10-804-491-4 Sequence 4, Appli
4	1449	100.0	281	4	US-10-804-491-46 Sequence 46, Appl
5	893	61.6	278	3	US-09-918-715-178 Sequence 178, App
6	893	61.6	278	4	US-10-804-491-41 Sequence 41, Appl
7	893	61.6	278	4	US-10-474-794-178 Sequence 178, App
8	893	61.6	278	5	US-10-723-860-459 Sequence 459, App
9	893	61.6	278	5	US-10-979-159-178 Sequence 178, App
10	889	61.4	266	3	US-09-778-963A-4 Sequence 4, Appli
11	889	61.4	266	3	US-09-918-715-198 Sequence 198, App
12	889	61.4	266	4	US-10-474-794-198 Sequence 198, App
13	889	61.4	266	5	US-10-979-159-198 Sequence 198, App
14	879	60.7	266	3	US-09-778-963A-2 Sequence 2, Appli
15	863	59.6	266	3	US-09-778-963A-5 Sequence 5, Appli
16	863	59.6	266	3	US-09-918-715-293 Sequence 293, App
17	863	59.6	266	4	US-10-474-794-293 Sequence 293, App
18	863	59.6	266	5	US-10-979-159-293 Sequence 293, App
19	719	49.6	293	5	US-10-450-763-56743 Sequence 56743, A
20	615	42.4	434	6	US-11-097-143-8925 Sequence 8925, Ap
21	517	35.7	175	4	US-10-029-386-32557 Sequence 32557, A
22	334	23.1	199	4	US-10-399-456-16 Sequence 16, Appl
23	330.5	22.8	319	6	US-11-097-143-31053 Sequence 31053, A
24	326	22.5	198	3	US-09-873-546-5 Sequence 5, Appli

25	322	22.2	293	4	US-10-363-829-453	Sequence 453, App
26	307.5	21.2	233	6	US-11-097-143-18480	Sequence 18480, A
27	305	21.0	183	4	US-10-231-956A-429	Sequence 429, App
28	303	20.9	219	4	US-10-369-493-5393	Sequence 5393, Ap
29	301	20.8	183	3	US-09-482-520A-8	Sequence 8, Appli
30	301	20.8	183	3	US-09-873-546-12	Sequence 12, Appl
31	301	20.8	183	5	US-10-501-035-390	Sequence 390, App
32	301	20.8	203	4	US-10-197-666A-84	Sequence 84, Appl
33	301	20.8	204	4	US-10-197-666A-82	Sequence 82, Appl
34	301	20.8	204	4	US-10-408-765A-1241	Sequence 1241, Ap
35	301	20.8	204	4	US-10-322-281-474	Sequence 474, App
36	301	20.8	204	4	US-10-788-792-208	Sequence 208, App
37	301	20.8	204	4	US-10-788-792-209	Sequence 209, App
38	301	20.8	214	4	US-10-322-281-467	Sequence 467, App
39	301	20.8	288	4	US-10-106-698-5350	Sequence 5350, Ap
40	301	20.8	734	4	US-10-344-404-31	Sequence 31, Appl
41	301	20.8	758	4	US-10-344-404-36	Sequence 36, Appl
42	300	20.7	183	4	US-10-755-889-82	Sequence 82, Appl
43	300	20.7	190	3	US-09-764-868-680	Sequence 680, App
44	299.5	20.7	745	4	US-10-344-404-19	Sequence 19, Appl
45	291	20.1	175	3	US-09-764-868-1103	Sequence 1103, Ap

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OM protein - protein search, using sw model

Run on: July 26, 2006, 11:11:26 ; Search time 32 Seconds
(without alignments)
579.950 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	301	20.8	204	6	US-10-539-228-474 Sequence 474, App
2	301	20.8	214	6	US-10-539-228-467 Sequence 467, App
3	283.5	19.6	184	6	US-10-539-228-78 Sequence 78, Appl
4	282.5	19.5	184	6	US-10-539-228-822 Sequence 822, App
5	282	19.5	218	6	US-10-505-928-636 Sequence 636, App
6	282	19.5	218	6	US-10-505-928-640 Sequence 640, App
7	279.5	19.3	227	6	US-10-449-902-38336 Sequence 38336, A
8	279	19.3	212	7	US-11-056-355B-56721 Sequence 56721, A
9	274.5	18.9	165	6	US-10-539-228-71 Sequence 71, Appl
10	263	18.2	508	6	US-10-449-902-41537 Sequence 41537, A
11	250	17.3	256	6	US-10-539-228-472 Sequence 472, App
12	249	17.2	171	6	US-10-539-228-470 Sequence 470, App
13	216	14.9	214	7	US-11-056-355B-83401 Sequence 83401, A
14	203	14.0	207	7	US-11-056-355B-79468 Sequence 79468, A
15	200.5	13.8	203	6	US-10-449-902-37725 Sequence 37725, A
16	197	13.6	208	7	US-11-056-355B-24978 Sequence 24978, A
17	197	13.6	208	7	US-11-056-355B-85480 Sequence 85480, A
18	197	13.6	221	6	US-10-449-902-32778 Sequence 32778, A
19	197	13.6	221	6	US-10-449-902-42945 Sequence 42945, A
20	194	13.4	257	6	US-10-953-349-7834 Sequence 7834, Ap
21	189.5	13.1	221	6	US-10-449-902-50932 Sequence 50932, A
22	188	13.0	207	6	US-10-953-349-25154 Sequence 25154, A

23	188	13.0	207	7	US-11-056-355B-59234	Sequence 59234, A
24	187	12.9	221	6	US-10-953-349-7835	Sequence 7835, Ap
25	186	12.8	294	7	US-11-330-403-10145	Sequence 10145, A
26	184	12.7	214	6	US-10-449-902-39420	Sequence 39420, A
27	184	12.7	260	6	US-10-953-349-34139	Sequence 34139, A
28	184	12.7	260	7	US-11-056-355B-5833	Sequence 5833, Ap
29	183.5	12.7	198	6	US-10-953-349-3072	Sequence 3072, Ap
30	183.5	12.7	198	7	US-11-056-355B-30837	Sequence 30837, A
31	183.5	12.7	198	7	US-11-056-355B-34427	Sequence 34427, A
32	183.5	12.7	198	7	US-11-056-355B-76335	Sequence 76335, A
33	182.5	12.6	198	6	US-10-566-644-170	Sequence 170, App
34	182.5	12.6	198	7	US-11-056-355B-76565	Sequence 76565, A
35	182	12.6	203	7	US-11-056-355B-82742	Sequence 82742, A
36	182	12.6	252	7	US-11-056-355B-82741	Sequence 82741, A
37	180.5	12.5	133	6	US-10-539-228-76	Sequence 76, Appl
38	180.5	12.5	193	6	US-10-566-644-206	Sequence 206, App
39	180	12.4	198	6	US-10-566-644-230	Sequence 230, App
40	180	12.4	201	6	US-10-953-349-34141	Sequence 34141, A
41	180	12.4	201	7	US-11-056-355B-5835	Sequence 5835, Ap
42	180	12.4	201	7	US-11-056-355B-10240	Sequence 10240, A
43	180	12.4	206	7	US-11-056-355B-28710	Sequence 28710, A
44	180	12.4	206	7	US-11-056-355B-32300	Sequence 32300, A
45	180	12.4	207	6	US-10-953-349-34140	Sequence 34140, A

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OM protein - protein search, using sw model

Run on: July 26, 2006, 10:54:01 ; Search time 40 Seconds
(without alignments)
675.923 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	314.5	21.7	217	1 TVWYRS	transforming prote
2	306	21.1	183	1 TVHUR2	transforming prote
3	303	20.9	219	2 T15833	hypothetical prote
4	301	20.8	183	2 S03180	transforming prote
5	301	20.8	203	1 TVHUC2	GTP-binding protei
6	296.5	20.5	215	2 JN0562	hypothetical 24K p
7	290.5	20.0	219	2 T45545	transforming prote
8	289.5	20.0	188	2 S65761	ras-related GTP-bi
9	288.5	19.9	219	1 TVBYSR	transforming prote
10	288.5	19.9	425	2 T25549	hypothetical prote
11	287	19.8	186	2 A37355	transforming prote
12	286.5	19.8	192	2 S32042	GTP-binding protei
13	285.5	19.7	186	1 TVDORS	transforming prote
14	285.5	19.7	186	2 S11229	GTP-binding protei
15	285.5	19.7	212	2 A53778	GTP-binding protei
16	283.5	19.6	184	1 A34655	transforming prote
17	283.5	19.6	184	1 TVHUR1	transforming prote
18	283.5	19.6	184	2 F38625	GTP-binding protei
19	283.5	19.6	184	2 A61216	transforming prote
20	283	19.5	188	1 TVMS2K	transforming prote
21	283	19.5	188	2 S34138	transforming prote
22	283	19.5	272	2 A34511	GTP-binding protei
23	282.5	19.5	184	1 A31961	transforming prote
24	282.5	19.5	184	2 A32342	transforming prote
25	282	19.5	188	2 I58402	transforming prote
26	282	19.5	218	1 TVHURR	transforming prote

27	281	19.4	188	2	JC5154	K-ras protein - tu
28	281	19.4	213	2	S12892	transforming prote
29	280.5	19.4	184	2	A41217	transforming prote
30	280	19.3	188	1	TVHU2K	transforming prote
31	280	19.3	188	2	S31720	transforming prote
32	279.5	19.3	193	2	S38362	Ppras2 protein - s
33	279	19.3	219	1	TVBYPR	ras-like protein 1
34	278.5	19.2	184	2	JC5155	rap1A protein - tu
35	276	19.0	188	2	T19507	hypothetical prote
36	275.5	19.0	189	1	TVCHRS	transforming prote
37	275.5	19.0	189	1	TVHUH	transforming prote
38	274.5	18.9	189	1	TVMVNS	transforming prote
39	274.5	18.9	241	1	TVMV3H	transforming prote
40	274	18.9	189	2	S33796	ras protein homolo
41	273.5	18.9	172	2	A54321	transforming prote
42	273.5	18.9	183	2	S05483	transforming prote
43	273.5	18.9	189	2	A43816	transforming prote
44	273.5	18.9	189	2	A25229	c-H-ras 1 protein
45	272.5	18.8	187	2	A60192	transforming prote

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-2.rup.

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OM protein - protein search, using sw model

Run on: July 26, 2006, 10:50:36 ; Search time 297 Seconds
(without alignments)
875.183 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMKCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	281	1 RASD1_HUMAN	Q9y272 homo sapien
2	1405.5	97.0	280	1 RASD1_MOUSE	O35626 mus musculu
3	1405.5	97.0	280	2 Q5SWR8_MOUSE	Q5swr8 mus musculu
4	1399.5	96.6	280	1 RASD1_RAT	Q9jkl8 rattus norv
5	1399.5	96.6	280	2 Q4KLL2_RAT	Q4kl12 rattus norv
6	1242.5	85.7	275	2 Q3SZ02_BOVIN	Q3sz02 bos taurus
7	1164	80.3	264	2 Q66IP2_XENLA	Q66ip2 xenopus lae
8	1144.5	79.0	265	2 Q6PHV8_BRARE	Q6phv8 brachydanio
9	1106	76.3	266	2 Q4SQU1_TETNG	Q4squl tetraodon n
10	1052.5	72.6	265	2 Q4SGP0_TETNG	Q4sgp0 tetraodon n
11	996	68.7	194	2 Q9HC43_HUMAN	Q9hc43 homo sapien
12	896	61.8	266	2 Q6GM99_XENLA	Q6gm99 xenopus lae
13	889	61.4	266	1 RHES_HUMAN	Q96d21 homo sapien
14	867	59.8	317	2 Q8JZW1_MOUSE	Q8jzw1 mus musculu
15	863	59.6	266	1 RHES_MOUSE	P63032 mus musculu
16	863	59.6	266	1 RHES_RAT	P63033 rattus norv
17	615	42.4	419	2 Q2M0S8_DROPS	Q2m0s8 drosophila
18	615	42.4	434	2 Q9VS10_DROME	Q9vs10 drosophila
19	514	35.5	335	2 Q4V8V9_BRARE	Q4v8v9 brachydanio
20	503.5	34.7	290	2 Q4SE27_TETNG	Q4se27 tetraodon n
21	367.5	25.4	208	2 Q5XWT8_BRARE	Q5xwt8 brachydanio
22	359.5	24.8	208	2 Q2LIW7_FUGRU	Q2liw7 fugu rubrip
23	359	24.8	306	2 Q9W5G7_DROME	Q9w5g7 drosophila
24	355.5	24.5	208	2 Q2LIW5_GASAC	Q2liw5 gasterosteu
25	350.5	24.2	216	2 Q2LIW4_ONCMY	Q2liw4 oncorhynch
26	347.5	24.0	208	2 Q5XWT6_CHICK	Q5xwt6 gallus gall
27	343.5	23.7	206	2 Q4S9K3_TETNG	Q4s9k3 tetraodon n
28	343.5	23.7	208	2 Q2LIW3_ORYLA	Q2liw3 oryzias lat

29	341	23.5	199	2	Q6GM41_XENLA	Q6gm41 xenopus lae
30	339	23.4	195	2	Q803Y2_BRARE	Q803y2 brachydanio
31	336.5	23.2	206	2	Q2LIW6_FUGRU	Q2liw6 fugu rubrip
32	335	23.1	199	1	DIRA2_MACFA	Q95kd9 macaca fasc
33	335	23.1	199	1	DIRA2_PONPY	Q5r6s2 pongo pygma
34	334.5	23.1	211	2	Q2LIW9_BRARE	Q2liw9 brachydanio
35	334	23.1	199	1	DIRA2_HUMAN	Q96hu8 homo sapien
36	334	23.1	199	1	DIRA2_MOUSE	Q5pr73 mus musculu
37	334	23.1	199	2	Q3UWU7_MOUSE	Q3uwu7 m in vitro
38	333.5	23.0	243	2	Q7QH99_ANOGA	Q7qh99 anopheles g
39	331	22.8	198	2	Q5PQ55_XENLA	Q5pq55 xenopus lae
40	328	22.6	198	2	Q4RMS0_TETNG	Q4rms0 tetraodon n
41	326	22.5	198	1	DIRA1_HUMAN	O95057 homo sapien
42	325.5	22.5	280	2	Q9V986_DROME	Q9v986 drosophila
43	321	22.2	198	1	DIRA1_MOUSE	Q91z61 mus musculu
44	318.5	22.0	280	2	Q8MQJ0_DROME	Q8mqj0 drosophila
45	314.5	21.7	217	1	RAS_LENED	P28775 lentinula e

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-25.p2n.rge.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:34 ; Search time 4373.38 Seconds
(without alignments)
3969.861 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100916_16816/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10804491_CGN_1_1_6250@runat_26072006_100916_16816 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID	Description	

1	931	100.0	546	5	AF493929	AF493929 Homo sapi
2	931	100.0	744	2	AR075100	AR075100 Sequence
3	931	100.0	744	2	BD091623	BD091623 Human reg
4	931	100.0	1285	5	AF030108	AF030108 Homo sapi
5	931	100.0	1691	2	AR534285	AR534285 Sequence
6	931	100.0	1691	2	AR544571	AR544571 Sequence
7	931	100.0	1691	5	AF159570	AF159570 Homo sapi
8	931	100.0	1710	5	BC030059	BC030059 Homo sapi
9	931	100.0	1923	2	BD074349	BD074349 50 human
10	931	100.0	2075	2	CQ714475	CQ714475 Sequence
11	931	100.0	2076	5	AB008109	AB008109 Homo sapi
12	931	100.0	2190	2	AR380250	AR380250 Sequence
13	931	100.0	2601	7	BV180396	BV180396 sqnm10933
14	931	100.0	5683	5	HSM805729	BX537427 Homo sapi
15	918	98.6	1802	5	AB169604	AB169604 Macaca fa
16	918	98.6	3208	2	AR454638	AR454638 Sequence
17	915	98.3	955	2	BD021618	BD021618 Novel gen
18	915	98.3	955	2	BD101556	BD101556 Novel gen
19	862	92.6	2173	14	BC102265	BC102265 Bos tauru
20	855	91.8	2078	14	SSC549925	AJ549925 Sus scrof
21	843	90.5	1812	6	BC037683	BC037683 Mus muscu
22	838	90.0	543	2	BD168778	BD168778 New disea
23	838	90.0	543	2	BD183821	BD183821 New disea
24	838	90.0	546	6	AF241259	AF241259 Rattus no
25	838	90.0	817	2	BD168782	BD168782 New disea
26	838	90.0	817	2	BD183825	BD183825 New disea
27	833	89.5	2397	6	MMU67188	U67188 Mus musculu
28	788	84.6	1219	11	BX931079	BX931079 Gallus ga
29	767	82.4	4487	11	BC077275	BC077275 Xenopus l
30	680.5	73.1	2765	11	BC054594	BC054594 Danio rer
31	661	71.0	663	2	DD208725	DD208725 THERAPEUT
32	576	61.9	373	5	AJ891044	AJ891044 Homo sapi
33	510	54.8	2112	11	BX950639	BX950639 Gallus ga
34	499	53.6	618	5	AF493928	AF493928 Homo sapi
35	499	53.6	618	5	BT007025	BT007025 Homo sapi
36	499	53.6	618	8	AY889515	AY889515 Synthetic
37	499	53.6	618	8	AY889516	AY889516 Synthetic
38	499	53.6	618	8	AY891976	AY891976 Synthetic
39	499	53.6	618	8	AY891977	AY891977 Synthetic
40	499	53.6	618	8	BT007756	BT007756 Synthetic
41	499	53.6	800	2	AR270528	AR270528 Sequence
42	499	53.6	800	5	HSU27768	U27768 Human RGP4
43	499	53.6	840	2	CQ714476	CQ714476 Sequence
44	499	53.6	1238	2	CQ434203	CQ434203 Sequence
45	499	53.6	1869	5	BC000737	BC000737 Homo sapi

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-25.p2n.rng.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:08:51 ; Search time 478.357 Seconds
(without alignments)
3957.222 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100914_16805/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491 @CGN_1_1_942 @runat_26072006_100914_16805 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				ID	Description
No.	Score	Match	Length	DB			

1	931	100.0	745	2	AAV38084	Aav38084 Human reg
2	931	100.0	1691	3	AAZ36910	Aaz36910 cDNA enco
3	931	100.0	1923	2	AAX51745	Aax51745 DNA encod
4	931	100.0	1923	6	ABQ92597	Abq92597 Human sec
5	931	100.0	2075	10	ABX74396	Abx74396 Human cDN
6	931	100.0	2076	11	ADP65641	Adp65641 Human mRN
7	931	100.0	2076	11	ADP65077	Adp65077 Human reg
8	931	100.0	2076	13	ACN37542	Acn37542 Tumour-as
9	931	100.0	2190	11	ADI31469	Adi31469 Human cDN
10	931	100.0	2190	13	ADS83536	Ads83536 Human lym
11	918	98.6	3208	12	ADI61743	Adi61743 Human cDN
12	918	98.6	3208	14	AEA43908	Aea43908 Human cDN
13	918	98.6	5809	10	ADI02562	Adi02562 Human cDN
14	915	98.3	955	4	AAI97781	Aai97781 Human neu
15	838	90.0	543	6	ABL99975	Abl99975 Rat disea
16	838	90.0	546	13	ADV41196	Adv41196 Rat cardi
17	838	90.0	817	6	ABL99979	Abl99979 Rat disea
18	661	71.0	663	10	ADF44700	Adf44700 Human NOV
19	645	69.3	663	12	ADO50885	Ado50885 Human NOV
20	637	68.4	459	9	ACH26489	Ach26489 Human adu
21	591	63.5	425	14	ACL56764	AcL56764 Human col
22	584	62.7	411	9	ACH29910	Ach29910 Human tes
23	499	53.6	753	11	ADN95589	Adn95589 Human BEC
24	499	53.6	753	14	ADX25911	Adx25911 Novel cel
25	499	53.6	800	10	ACA56493	Aca56493 Human sig
26	499	53.6	800	12	ADI56289	Adi56289 Human pol
27	499	53.6	1238	4	AAL26766	Aal26766 Human bre
28	499	53.6	1531	11	ACN88713	Acn88713 Breast ca
29	499	53.6	1869	13	ADV35068	Adv35068 Human cDN
c 30	499	53.6	2752	11	ACN92693	Acn92693 Breast ca
31	499	53.6	2753	14	ADX97767	Adx97767 Human reg
32	499	53.6	2769	12	ADP21408	Adp21408 Gene RGS4
33	499	53.6	2934	6	ABK47336	Abk47336 cDNA enco
34	499	53.6	2981	14	AED14119	Aed14119 Human cum
35	499	53.6	3165	8	ABX63113	Abx63113 Human cDN
36	499	53.6	3167	10	ADD12660	Add12660 Human cDN
37	497	53.4	1489	14	ADX25668	Adx25668 Novel cel
38	497	53.4	2919	14	ADX26148	Adx26148 Novel cel
c 39	496	53.3	558	10	ADB57446	Adb57446 Toxicity-
40	494	53.1	2781	14	ADX26006	Adx26006 Novel cel
41	463.5	49.8	2383	2	AAT11418	Aat11418 p53 respo
42	463.5	49.8	2383	8	ACF12929	Acf12929 Human cer
43	463.5	49.8	2383	10	ADK61425	Adk61425 Ovarian c
44	463.5	49.8	2383	11	ADN95175	Adn95175 Human BEC
45	463.5	49.8	2383	12	ADO19709	Ado19709 Human PRO

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-25.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:01 ; Search time 144.957 Seconds
(without alignments)
3504.536 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100921_16893/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss05h -USER=US10804491_CGN_1_1_252@runat_26072006_100921_16893
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	931	100.0	744	2	US-08-748-483-2 Sequence 2, Appli
2	931	100.0	1691	3	US-09-709-103-24 Sequence 24, Appl
3	931	100.0	1691	3	US-09-439-410A-24 Sequence 24, Appl
4	931	100.0	2075	3	US-09-949-016-5328 Sequence 5328, Ap
5	931	100.0	2190	3	US-09-023-655-795 Sequence 795, App

6	918	98.6	3208	3	US-09-566-921-111	Sequence 111, App
7	499	53.6	733	3	US-09-949-016-5329	Sequence 5329, Ap
8	499	53.6	800	3	US-09-016-434-1091	Sequence 1091, Ap
9	463.5	49.8	2383	2	US-08-274-318-1	Sequence 1, Appli
10	463.5	49.8	2383	2	US-08-754-108-1	Sequence 1, Appli
11	463.5	49.8	2383	3	US-09-949-016-419	Sequence 419, App
12	462.5	49.7	606	2	US-08-463-081B-27	Sequence 27, Appl
13	462.5	49.7	606	2	US-08-461-379A-27	Sequence 27, Appl
14	462.5	49.7	606	2	US-08-462-390B-27	Sequence 27, Appl
15	462.5	49.7	606	3	US-08-463-074B-27	Sequence 27, Appl
16	462.5	49.7	606	3	US-08-465-585C-27	Sequence 27, Appl
17	462.5	49.7	606	3	US-08-652-446-27	Sequence 27, Appl
18	462.5	49.7	746	3	US-08-870-815-3	Sequence 3, Appli
19	462.5	49.7	746	3	US-08-949-004-3	Sequence 3, Appli
20	462.5	49.7	2370	3	US-09-949-016-1870	Sequence 1870, Ap
21	462.5	49.7	2406	2	US-08-463-081B-1	Sequence 1, Appli
22	462.5	49.7	2406	2	US-08-461-379A-1	Sequence 1, Appli
23	462.5	49.7	2406	2	US-08-462-390B-1	Sequence 1, Appli
24	462.5	49.7	2406	3	US-08-463-074B-1	Sequence 1, Appli
25	462.5	49.7	2406	3	US-08-465-585C-1	Sequence 1, Appli
26	462.5	49.7	2406	3	US-08-652-446-1	Sequence 1, Appli
27	461	49.5	939	3	US-09-799-451-353	Sequence 353, App
28	447	48.0	2272	2	US-08-726-228-1	Sequence 1, Appli
29	447	48.0	2272	3	US-08-870-815-1	Sequence 1, Appli
30	447	48.0	2272	3	US-08-949-004-1	Sequence 1, Appli
31	445.5	47.9	1697	4	US-10-094-749-11	Sequence 11, Appl
32	440.5	47.3	2637	3	US-09-949-016-4047	Sequence 4047, Ap
33	440.5	47.3	2638	3	US-09-016-434-1090	Sequence 1090, Ap
34	427.5	45.9	1164	3	US-09-244-314-3	Sequence 3, Appli
35	427.5	45.9	1164	3	US-09-498-959-3	Sequence 3, Appli
36	427.5	45.9	1164	3	US-09-894-749-3	Sequence 3, Appli
37	423	45.4	2874	5	US-10-114-270-151	Sequence 151, App
38	421.5	45.3	2217	3	US-09-244-314-1	Sequence 1, Appli
39	421.5	45.3	2217	3	US-09-498-959-1	Sequence 1, Appli
40	421.5	45.3	2217	3	US-09-894-749-1	Sequence 1, Appli
41	415.5	44.6	1345	3	US-09-016-434-1278	Sequence 1278, Ap
42	415.5	44.6	1345	3	US-09-023-655-1243	Sequence 1243, Ap
43	415.5	44.6	1345	3	US-09-949-016-417	Sequence 417, App
44	415.5	44.6	1345	3	US-09-949-016-4737	Sequence 4737, Ap
45	351.5	37.8	1226	3	US-09-949-016-4736	Sequence 4736, Ap

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-25.p2n.rnpbm.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 15:25:55 ; Search time 966.9 Seconds
(without alignments)
3450.296 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100930_17074/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491@CGN_1_1_2326@runat_26072006_100930_17074 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	%
Result	Query

No.	Score	Match	Length	DB	ID	Description
1	931	100.0	744	3	US-09-206-639-2	Sequence 2, Appli
2	931	100.0	1691	9	US-10-804-491-24	Sequence 24, Appl
3	931	100.0	1923	7	US-10-411-224-55	Sequence 55, Appl
4	931	100.0	1923	7	US-10-047-021-55	Sequence 55, Appl
5	931	100.0	1923	10	US-10-970-493-55	Sequence 55, Appl
6	931	100.0	2076	8	US-10-240-425-345	Sequence 345, App
7	931	100.0	2076	10	US-10-956-157-1090	Sequence 1090, Ap
8	931	100.0	2076	10	US-10-287-436A-174	Sequence 174, App
9	931	100.0	2076	10	US-10-287-436A-784	Sequence 784, App
10	931	100.0	2190	8	US-10-641-643-795	Sequence 795, App
11	918	98.6	3208	10	US-10-765-700-111	Sequence 111, App
12	918	98.6	5809	7	US-10-133-013-103	Sequence 103, App
13	838	90.0	543	7	US-10-398-953-2	Sequence 2, Appli
14	838	90.0	817	7	US-10-398-953-6	Sequence 6, Appli
15	763	82.0	1811	16	US-11-136-527-2529	Sequence 2529, Ap
16	661	71.0	663	8	US-10-357-820-47	Sequence 47, Appl
17	637	68.4	459	3	US-09-918-995-13701	Sequence 13701, A
18	584	62.7	411	3	US-09-918-995-17122	Sequence 17122, A
19	499	53.6	800	7	US-10-305-720-1091	Sequence 1091, Ap
20	499	53.6	1531	6	US-10-198-846-9863	Sequence 9863, Ap
21	499	53.6	1869	6	US-10-175-523-144	Sequence 144, App
22	499	53.6	1869	13	US-11-099-266-144	Sequence 144, App
c 23	499	53.6	2752	6	US-10-198-846-13843	Sequence 13843, A
24	499	53.6	2934	3	US-09-939-209A-1	Sequence 1, Appli
25	499	53.6	2981	16	US-11-091-883-133	Sequence 133, App
26	499	53.6	3165	6	US-10-044-090-113	Sequence 113, App
27	499	53.6	3167	3	US-09-918-624B-6	Sequence 6, Appli
28	483	51.9	3003	16	US-11-136-527-2384	Sequence 2384, Ap
29	463.5	49.8	2383	6	US-10-171-311-201	Sequence 201, App
30	463.5	49.8	2383	7	US-10-159-563-311	Sequence 311, App
31	463.5	49.8	2383	10	US-10-505-680-595	Sequence 595, App
32	462.5	49.7	746	3	US-09-873-438-3	Sequence 3, Appli
33	462.5	49.7	875	8	US-10-755-889-7	Sequence 7, Appli
34	462.5	49.7	2434	7	US-10-240-965-112	Sequence 112, App
35	462.5	49.7	2883	9	US-10-723-860-6606	Sequence 6606, Ap
36	461	49.5	939	8	US-10-302-172-353	Sequence 353, App
37	459	49.3	540	6	US-10-275-555-1	Sequence 1, Appli
38	458	49.2	3494	16	US-11-136-527-2531	Sequence 2531, Ap
39	447	48.0	2272	3	US-09-873-438-1	Sequence 1, Appli
40	445.5	47.9	1697	7	US-10-094-749-11	Sequence 11, Appl
41	444.5	47.7	3594	6	US-10-087-192-1727	Sequence 1727, Ap
42	443	47.6	1283	3	US-09-814-353-19578	Sequence 19578, A
43	440.5	47.3	1400	10	US-10-956-157-7580	Sequence 7580, Ap
44	440.5	47.3	2623	7	US-10-108-260A-1527	Sequence 1527, Ap
45	440.5	47.3	2638	3	US-09-954-456-1955	Sequence 1955, Ap

This page gives you Search Results detail for the Application 10804491 and Search Result us-10-804-491-25.p2n.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:39 ; Search time 3683.86 Seconds
(without alignments)
4121.248 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100918_16839/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10804491 @CGN_1_1_7986 @runat_26072006_100918_16839 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	931	100.0	558	9	DA135142	DA135142 DA135142

2	931	100.0	583	4	CA773163	CA773163	im60e01.y
3	931	100.0	584	5	CK818116	CK818116	ic19d08.x
4	931	100.0	585	4	CA948732	CA948732	iq27a04.y
5	931	100.0	603	8	CV573520	CV573520	od37b08.y
6	931	100.0	614	4	CA951023	CA951023	ir93h02.y
7	931	100.0	627	9	DA131516	DA131516	DA131516
8	931	100.0	631	2	BM503802	BM503802	ig96a05.y
9	931	100.0	632	3	BQ776798	BQ776798	il33d02.y
10	931	100.0	633	4	CA841290	CA841290	ip32c06.y
11	931	100.0	641	2	BI713756	BI713756	ie03f03.y
12	931	100.0	645	4	CA394466	CA394466	cs51h05.y
13	931	100.0	645	4	CA397513	CA397513	cs92a10.y
14	931	100.0	651	4	CB053503	CB053503	NISC_g114
15	931	100.0	653	3	BU785180	BU785180	in42a09.y
16	931	100.0	661	7	BE890175	BE890175	601513155
17	931	100.0	695	8	CN268954	CN268954	170006000
18	931	100.0	696	1	AU139601	AU139601	AU139601
19	931	100.0	708	4	CA407266	CA407266	1003415 H
20	931	100.0	708	5	CD242148	CD242148	AGENCOURT
21	931	100.0	714	4	CB962876	CB962876	AGENCOURT
22	931	100.0	718	4	CA391795	CA391795	cs19a01.y
23	931	100.0	722	4	CB962581	CB962581	AGENCOURT
24	931	100.0	733	3	BU539966	BU539966	AGENCOURT
25	931	100.0	734	5	CD299504	CD299504	AGENCOURT
26	931	100.0	734	5	CD357245	CD357245	AGENCOURT
27	931	100.0	737	2	BI770010	BI770010	603053514
28	931	100.0	737	4	CD000470	CD000470	AGENCOURT
29	931	100.0	738	5	CD299098	CD299098	AGENCOURT
30	931	100.0	740	4	CD110719	CD110719	AGENCOURT
31	931	100.0	742	8	CN268951	CN268951	170005321
32	931	100.0	744	5	CD511422	CD511422	AGENCOURT
33	931	100.0	746	4	CB963796	CB963796	AGENCOURT
34	931	100.0	746	5	CD250671	CD250671	AGENCOURT
35	931	100.0	748	2	BG708234	BG708234	602671755
36	931	100.0	748	5	CD299067	CD299067	AGENCOURT
37	931	100.0	749	1	AU138261	AU138261	AU138261
38	931	100.0	751	4	CB962349	CB962349	AGENCOURT
39	931	100.0	752	5	CD511204	CD511204	AGENCOURT
40	931	100.0	753	4	CB963300	CB963300	AGENCOURT
41	931	100.0	756	4	CB963443	CB963443	AGENCOURT
42	931	100.0	757	5	CD241903	CD241903	AGENCOURT
43	931	100.0	758	5	CD356513	CD356513	AGENCOURT
44	931	100.0	759	4	CB962257	CB962257	AGENCOURT
45	931	100.0	762	5	CD356626	CD356626	AGENCOURT

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OM protein - protein search, using sw model

Run on: July 26, 2006, 10:49:51 ; Search time 199 Seconds
(without alignments)
645.617 Million cell updates/sec

Title: US-10-804-491-2
Perfect score: 1449
Sequence: 1 MKLAAMIKMCPDSELSIP.....IREKASAGSQAKDKERCVIS 281

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1449	100.0	281	2 AAY42693	Aay42693 Human kd3
2	1449	100.0	281	3 AAY53924	Aay53924 An activa
3	1449	100.0	281	3 AAY53921	Aay53921 A human a
4	1449	100.0	281	6 ABR41059	Abr41059 Human MAP
5	1449	100.0	281	8 ADU06635	Adu06635 Novel bro
6	1441	99.4	281	3 AAY99656	Aay99656 Human GTP
7	1399.5	96.6	280	2 AAY42694	Aay42694 Rat kd312
8	893	61.6	278	3 AAY53923	Aay53923 A homolog
9	893	61.6	278	5 ABB90722	Abb90722 Human Tum
10	893	61.6	278	6 ABU54429	Abu54429 Human tum
11	893	61.6	278	8 ADI67005	Adi67005 Human DEX
12	893	61.6	278	8 ADQ17642	Adq17642 Human sof
13	893	61.6	407	5 ABG59971	Abg59971 Human DIT
14	889	61.4	266	5 ABB90733	Abb90733 Human Tum
15	889	61.4	266	6 ABU54440	Abu54440 Human tum
16	879	60.7	266	5 ABG70951	Abg70951 Human Ras
17	863	59.6	266	5 ABB90781	Abb90781 Mouse Tum
18	863	59.6	266	6 ABU54488	Abu54488 Mouse tum
19	719	49.6	293	4 ABG26384	Abg26384 Novel hum
20	615	42.4	434	4 ABB60711	Abb60711 Drosophil

21	517	35.7	175	8	ABO58923	Abo58923	Human	gen
22	425	29.3	82	7	ADC35028	Adc35028	Ras-like	
23	334	23.1	199	4	AAM39896	Aam39896	Human	pol
24	334	23.1	199	5	AAE23389	Aae23389	Human	int
25	334	23.1	206	4	AAM41682	Aam41682	Human	pol
26	330.5	22.8	319	4	ABB68087	Abb68087	Drosophil	
27	327	22.6	214	7	ADE09235	Ade09235	Novel	pro
28	326	22.5	198	6	ABU62878	Abu62878	Human	ras
29	326	22.5	238	6	ABU11837	Abu11837	Human	MDD
30	326	22.5	253	7	ADE08246	Ade08246	Novel	pro
31	322	22.2	293	5	ABP51431	Abp51431	Human	MDD
32	307.5	21.2	233	4	ABB63896	Abb63896	Drosophil	
33	305	21.0	183	8	ADL35821	Adl35821	Human	RAS
34	305	21.0	183	8	ADN05368	Adn05368	Antipsori	
35	305	21.0	215	4	AAM00956	Aam00956	Human	bon
36	303	20.9	219	8	ADN22740	Adn22740	Bacterial	
37	301	20.8	183	2	AAR05076	Aar05076	RAP1A	Gen
38	301	20.8	183	4	AAM39413	Aam39413	Human	pol
39	301	20.8	183	6	ABU62883	Abu62883	Ras-famil	
40	301	20.8	183	7	ADD14201	Add14201	Human	src
41	301	20.8	183	8	ADP24711	Adp24711	PRO	polyp
42	301	20.8	183	8	ADP25294	Adp25294	PRO	polyp
43	301	20.8	203	2	AAW82591	Aaw82591	Human	TC2
44	301	20.8	203	6	ABR41057	Abr41057	Human	MAP
45	301	20.8	204	6	ABR41056	Abr41056	Human	MAP

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 15:30:26 ; Search time 242.9 Seconds
(without alignments)
1708.556 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2187952 seqs, 764289321 residues

Total number of hits satisfying chosen parameters: 4375904

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100933_17116/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US10804491@CGN_1_1_278@runat_26072006_100933_17116 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
c 1	931	100.0	1017	8 US-11-266-748A-166427	Sequence 166427,
c 2	931	100.0	1019	8 US-11-266-748A-263637	Sequence 263637,
c 3	931	100.0	1019	8 US-11-266-748A-280028	Sequence 280028,
4	931	100.0	1019	8 US-11-266-748A-324154	Sequence 324154,
c 5	931	100.0	1056	8 US-11-266-748A-349794	Sequence 349794,

c	6	931	100.0	1056	8	US-11-266-748A-382515	Sequence 382515,
	7	931	100.0	1056	8	US-11-266-748A-433173	Sequence 433173,
c	8	931	100.0	1072	8	US-11-266-748A-15046	Sequence 15046, A
	9	931	100.0	1072	8	US-11-266-748A-64903	Sequence 64903, A
c	10	931	100.0	1072	8	US-11-266-748A-67735	Sequence 67735, A
c	11	931	100.0	1126	8	US-11-266-748A-84566	Sequence 84566, A
c	12	931	100.0	1126	8	US-11-266-748A-111881	Sequence 111881,
	13	931	100.0	1126	8	US-11-266-748A-137377	Sequence 137377,
c	14	931	100.0	1183	8	US-11-266-748A-349793	Sequence 349793,
c	15	931	100.0	1183	8	US-11-266-748A-382514	Sequence 382514,
	16	931	100.0	1183	8	US-11-266-748A-433172	Sequence 433172,
	17	931	100.0	2053	8	US-11-266-748A-185412	Sequence 185412,
	18	931	100.0	2053	8	US-11-266-748A-192910	Sequence 192910,
	19	931	100.0	2075	6	US-10-473-173-7	Sequence 7, Appli
	20	931	100.0	2076	8	US-11-266-748A-22313	Sequence 22313, A
c	21	927	99.6	848	8	US-11-266-748A-84567	Sequence 84567, A
c	22	927	99.6	848	8	US-11-266-748A-111882	Sequence 111882,
	23	927	99.6	848	8	US-11-266-748A-137378	Sequence 137378,
c	24	875	94.0	852	8	US-11-266-748A-166428	Sequence 166428,
c	25	875	94.0	852	8	US-11-266-748A-263638	Sequence 263638,
c	26	875	94.0	852	8	US-11-266-748A-280029	Sequence 280029,
	27	875	94.0	852	8	US-11-266-748A-324155	Sequence 324155,
	28	499	53.6	601	8	US-11-266-748A-54394	Sequence 54394, A
	29	499	53.6	753	6	US-10-505-928-512	Sequence 512, App
	30	463.5	49.8	2383	6	US-10-505-928-97	Sequence 97, Appl
c	31	462.5	49.7	826	8	US-11-266-748A-228623	Sequence 228623,
	32	462.5	49.7	826	8	US-11-266-748A-242801	Sequence 242801,
	33	462.5	49.7	831	8	US-11-266-748A-13171	Sequence 13171, A
	34	462.5	49.7	874	8	US-11-266-748A-365189	Sequence 365189,
c	35	462.5	49.7	874	8	US-11-266-748A-448568	Sequence 448568,
	36	462.5	49.7	884	8	US-11-266-748A-74509	Sequence 74509, A
c	37	462.5	49.7	884	8	US-11-266-748A-127320	Sequence 127320,
	38	462.5	49.7	2447	8	US-11-266-748A-56683	Sequence 56683, A
	39	444.5	47.7	948	8	US-11-266-748A-11251	Sequence 11251, A
	40	444.5	47.7	1502	8	US-11-266-748A-72435	Sequence 72435, A
c	41	444.5	47.7	1502	8	US-11-266-748A-125246	Sequence 125246,
	42	440.5	47.3	1274	8	US-11-266-748A-186909	Sequence 186909,
	43	440.5	47.3	2623	8	US-11-293-697-1527	Sequence 1527, Ap
	44	421.5	45.3	2164	8	US-11-266-748A-31114	Sequence 31114, A
	45	417	44.8	861	8	US-11-266-748A-175986	Sequence 175986,

SCORE Search Results Details for Application 10804491 and Search Result us-10-804-491-25.p2n.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2006, 10:09:39 ; Search time 3683.86 Seconds
(without alignments)
4121.248 Million cell updates/sec

Title: US-10-804-491-25
Perfect score: 931
Sequence: 1 MCKGLAALPHSCLERAKEIK.....MEKDSLPRFVRSEFYQELIK 181

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10804491/runat_26072006_100918_16839/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10804491@CGN_1_1_7986@runat_26072006_100918_16839 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*

13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	931	100.0	558	9	DA135142	DA135142 DA135142
2	931	100.0	583	4	CA773163	CA773163 im60e01.y
3	931	100.0	584	5	CK818116	CK818116 ic19d08.x
4	931	100.0	585	4	CA948732	CA948732 iq27a04.y
5	931	100.0	603	8	CV573520	CV573520 od37b08.y
6	931	100.0	614	4	CA951023	CA951023 ir93h02.y
7	931	100.0	627	9	DA131516	DA131516 DA131516
8	931	100.0	631	2	BM503802	BM503802 ig96a05.y
9	931	100.0	632	3	BQ776798	BQ776798 il33d02.y
10	931	100.0	633	4	CA841290	CA841290 ip32c06.y
11	931	100.0	641	2	BI713756	BI713756 ie03f03.y
12	931	100.0	645	4	CA394466	CA394466 cs51h05.y
13	931	100.0	645	4	CA397513	CA397513 cs92a10.y
14	931	100.0	651	4	CB053503	CB053503 NISC_gll4
15	931	100.0	653	3	BU785180	BU785180 in42a09.y
16	931	100.0	661	7	BE890175	BE890175 601513155
17	931	100.0	695	8	CN268954	CN268954 170006000
18	931	100.0	696	1	AU139601	AU139601 AU139601
19	931	100.0	708	4	CA407266	CA407266 1003415 H
20	931	100.0	708	5	CD242148	CD242148 AGENCOURT
21	931	100.0	714	4	CB962876	CB962876 AGENCOURT
22	931	100.0	718	4	CA391795	CA391795 cs19a01.y
23	931	100.0	722	4	CB962581	CB962581 AGENCOURT
24	931	100.0	733	3	BU539966	BU539966 AGENCOURT
25	931	100.0	734	5	CD299504	CD299504 AGENCOURT
26	931	100.0	734	5	CD357245	CD357245 AGENCOURT
27	931	100.0	737	2	BI770010	BI770010 603053514
28	931	100.0	737	4	CD000470	CD000470 AGENCOURT
29	931	100.0	738	5	CD299098	CD299098 AGENCOURT
30	931	100.0	740	4	CD110719	CD110719 AGENCOURT
31	931	100.0	742	8	CN268951	CN268951 170005321
32	931	100.0	744	5	CD511422	CD511422 AGENCOURT
33	931	100.0	746	4	CB963796	CB963796 AGENCOURT
34	931	100.0	746	5	CD250671	CD250671 AGENCOURT
35	931	100.0	748	2	BG708234	BG708234 602671755
36	931	100.0	748	5	CD299067	CD299067 AGENCOURT
37	931	100.0	749	1	AU138261	AU138261 AU138261
38	931	100.0	751	4	CB962349	CB962349 AGENCOURT
39	931	100.0	752	5	CD511204	CD511204 AGENCOURT
40	931	100.0	753	4	CB963300	CB963300 AGENCOURT
41	931	100.0	756	4	CB963443	CB963443 AGENCOURT
42	931	100.0	757	5	CD241903	CD241903 AGENCOURT
43	931	100.0	758	5	CD356513	CD356513 AGENCOURT
44	931	100.0	759	4	CB962257	CB962257 AGENCOURT
45	931	100.0	762	5	CD356626	CD356626 AGENCOURT

ALIGNMENTS

RESULT 1
DA135142
LOCUS DA135142 558 bp mRNA linear EST 01-NOV-2005
DEFINITION DA135142 BRALZ2 Homo sapiens cDNA clone BRALZ2007992 5', mRNA sequence.
ACCESSION DA135142
VERSION DA135142.1 GI:78560789
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 558)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,